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OM nucleic - nucleic search, using SW model

Run on: June 2, 2004, 16:46:28 ; Search time 131 Seconds
 (without alignments)
 3.962 Million cell updates/sec

Title: US-09-989-293A-376

Perfect score: 713
 Sequence: 1 aatatatcatctttatca.....tgttgcacaaagaaaaaaa 713

Scoring table: IDENTITY_NUC
 Gapext 0.5

Searched: 510 seqs, 363935 residues

Total number of hits satisfying chosen parameters: 1020

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 510 summaries

Database : rnpb376.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	713	100.0	713	1	US-09-989-722-376 Sequence 376, App
2	713	100.0	713	1	US-09-989-723-376 Sequence 376, App
3	713	100.0	713	1	US-09-989-729-376 Sequence 376, App
4	713	100.0	713	1	US-09-989-727-376 Sequence 376, App
5	713	100.0	713	1	US-09-989-731-376 Sequence 376, App
6	713	100.0	713	1	US-09-989-732-376 Sequence 376, App
7	713	100.0	713	1	US-09-991-073-376 Sequence 376, App
8	713	100.0	713	1	US-09-990-442-376 Sequence 376, App
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ALIGNMENTS

RESULT 1
 US-09-989-722-376
 Sequence 376, Application US/09989722
 / Patent No. US2002007267A1
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Godtstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Bacon, Dan L.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Watansabe, Colin K.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / APPLICANT: Zhang, Zemin

* PRIOR FILING DATE: 1999-08-25
 * PRIOR APPLICATION NUMBER: US 60/141,037
 * PRIOR FILING DATE: 1999-06-23
 * PRIOR APPLICATION NUMBER: US 60/092,182
 * PRIOR FILING DATE: 1998-07-09
 * NUMBER OF SEQ ID NOS: 532
 * SEQ ID NO: 376
 * LENGTH: 713
 * TYPE: DNA
 * ORGANISM: Homo sapiens
 * US-10-219-538-376

Query Match 100.0%; Score: 713; DB: 1; Length: 713;
 Best Local Similarity 100.0%; Pred. No.: 3.4;
 Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATATATCATATTATCATATAATGATTCTTCAATAACATTTGGG 60
 Db 1 ATATATCATATTATCATATAATGATTCTTCAATAACATTTGGG 60

QY 61 TTTCGGGATTAAATTCTAACACAGCAGATGACATTTCCTGTCACTATTATT 120
 Db 61 TTTCGGGATTAAATTCTAACACAGCAGATGACATTTCCTGTCACTATTATT 120

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QY 181 CTTCTCTATGAAATAAAGGAAACAGCTAACCCACAATCATCTTAGAGACAG 240
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QY 241 TGTGACTCTCCAACCAAGCTGCAAAACAGCTGCAACATGGCAAGGAAATCT 300
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QY 361 TTGAGTCAATGATGTTAAATTAAATGATTACCTTAGCTGTAAAT 420
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 Db 601 TTACAGAATGACATTTAATGCTGATTTAAATGCTGAAATGATGCTGAAAGG 660

QY 661 AAGAAATGACAGGAGAAAGGAAAGGAAATGTTGCAGGAAATGATGAAAGG 713
 Db 661 AAGAAATGACAGGAGAAAGGAAAGGAAATGTTGCAGGAAATGATGAAAGG 713

QY 713 AAGAAATGACATTTAATGCTGAAATGCTGAAATGATGCTGAAAGGAAAGG 713

RESULT 506
 US-10-147-528-473
 * Sequence 473, Application US/10147528
 ; Publication No. US2003219885A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura

```

RESULT 507
US-10-128-692A-473
; Sequence: 473, Application US/10128692A
; Publication No. US2010009547A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Inc.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gorski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tomas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: F3330RIC124
CURRENT APPLICATION NUMBER: US/10/128-692A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 550
SEQ ID NO 473
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-692A-473

Query Match
Best Local Similarity 100.0%; Score 713; DB 1; Length 713;
Matches 713; Conservative 0; Missmatches 0; Indels 0; Gaps 0;
; 1 AATATACATCTATTATCATTAATCATATAATGTTCAATACATTAACTTGGG 60
; 61 TTTCGGATTATTCAACAGGGAATGCAATTTCATTTCTTGTCTTATTATT 120
; 61 TTTCGGATTATTCAACAGGGAATGCAATTTCATTTCTTGTCTTATTATT 120
; 61 TTTCGGATTATTCAACAGGGAATGCAATTTCATTTCTTGTCTTATTATT 120

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QY	121	GTTGGTATGTGAGGTATTGGAGTCATTGGAGAAACATTTGGAGATGGCTA 180	
Db	121	GTTGGTATGTGAGGTATTGGAGAAACATTTGGAGATGGCTA 180	
QY	181	CTTCTCTATCAAGAAAATAAAGGAAACCCACGTGAAACCATCTTTAGAGACAG 240	
Db	181	CTTCTCTATCAAGAAAATAAAGGAAACCCACGTGAAACCATCTTTAGAGACAG 240	
QY	241	TGTGACTCTACCAAAAGCTGCAAACAGCAAGGGCATAGTTAAAGGAGGAATCT 300	
Db	241	TGTGACTCTACCAAAAGCTGCAAACAGCAAGGGCATAGTTAAAGGAGGAATCT 300	
QY	301	TGACTCAAGGGTTAATTCTTGTTGAGCTGGGCAAGGGTAAAGAAACAC 360	
Db	301	TGACTCAAGGGTTAATTCTTGTTGAGCTGGGCAAGGGTAAAGAAACAC 360	
QY	361	TTAGATTCAATGATTGAAATTAAAGCCTAACATATTAGTATTACCTTGTAT 420	
Db	361	T TAGATTCAATGATTGAAATTAAAGCCTAACATATTAGTATTACCTTGTAT 420	
QY	421	GTATCCCTGTCTATATAVACAATTAAGGTGAAATTAACTACCCATGGCTGGAC 480	
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Db	481	AGTTCTAAATGGACTTATAATTAAATCAGTAACCTGATTATCACTGGCTATCT 540	
QY	541	GCTTAAATCTCACGGGATCATATAATTGTATACAAATAAAAGAAATGTTCTCCCC 600	
Db	541	GCTTAAATCTCACGGGATCATATAATTGTATACAAATAAAAGAAATGTTCTCCCC 600	
QY	601	TTACAGATTGACATTAAATGCATACAGTTGAAATAGGAAATGACATTAAGG 660	
Db	601	TTACAGATTGACATTAAATGCATACAGTTGAAATAGGAAATGACATTAAGG 660	
QY	661	AAGAATGACAGGGAGAAAGGGAAAGGGGAAATGTGCCAAGGAAAAAA 713	
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RESULT 508			
US-10-140-927-473			
Sequence 473, Application US/10140927			
Publication No. US2004000958A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin P.			
APPLICANT: Beresini, Maureen			
APPLICANT: DeForge, Laura			
APPLICANT: Desnoyers, Luc			
APPLICANT: Filveroff, Ellen			
APPLICANT: Gao, Wei-Qiang			
APPLICANT: Gerritsen, Mary E.			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul J.			
APPLICANT: Gurney, Austin L.			
APPLICANT: Sherwood, Steven			
APPLICANT: Smith, Victoria			
APPLICANT: Stewart, Timothy A.			
APPLICANT: Tumas, Daniel			
APPLICANT: Watanabe, Colin K			
APPLICANT: Wood, William			
APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCBIC			
TITLE OF INVENTION: ACIDS ENCODING THE SAME			
FILE REFERENCE: P33301C180			
CURRENT APPLICATION NUMBER: US/10/140-927			
CURRENT FILING DATE: 2002-05-07			
PRIOR APPLICATION removed - See File Wrapper or Palm			
NUMBER OF SEQ ID NOS: 550			
SEQ ID NO 473			
LNPCTP: 713			

TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-927-473

Query Match Similarity 100.0%; Score 713; DB 1; Length 713;
Best Local Similarity 100.0%; Fred. No. 3.4;
Matches 713; Conservative 0; Mismatches 0; Gaps 0;

QY 1 AATATATCATCATTATCATATACTTAAAGTATTCATTCCAAATACATTGGG 60
Db 1 AATATATCATCATTATCATATACTTAAAGTATTCATTCCAAATACATTGGG 60

QY 61 TTGGGATTAAATTCAAAACAGAAGTAGACATTTCGTGCACATTATTATT 120
Db 61 TTGGGATTAAATTCAAAACAGAAGTAGACATTTCGTGCACATTATTATT 120

QY 121 GTGGATGTGAAGCTATTGGGATCCATTGGAGCACATGGGAATGGCTA 180
Db 121 GTGGATGTGAAGCTATTGGGATCCATTGGAGCACATGGGAATGGCTA 180

QY 181 CTTCTCTAAAGAAATAAGAACCAAGCAACATCATTTTGTCATTTATT 240
Db 181 CTTCTCTAAAGAAATAAGAACCAAGCAACATCATTTTGTCATTTATT 240

QY 241 TGTGACTCTTACCAAAAGCTGTCAAACACAGCAACATCATTTTGAGCAG 240
Db 241 TGTGACTCTTACCAAAAGCTGTCAAACACAGCAACATCATTTTGAGCAG 240

QY 301 TGAATCAGGGTTTAATCTGTGCTGAAGCTGGGAGGGTGTAAAGAAAAC 360
Db 301 TGAATCAGGGTTTAATCTGTGCTGAAGCTGGGAGGGTGTAAAGAAAAC 360

QY 361 TAGATTAATGATTGAAATTAGGAAATACATATTACCTAGTGAAT 420
Db 361 TAGATTAATGATTGAAATTAGGAAATACATATTACCTAGTGAAT 420

QY 421 GATCCCTGTCAATAATAGGTGAAATTAAAGCTTATGAGTGGCTGGAC 480
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QY 481 AGTCTAAATGGCTTAAATGGGAAACTGTTACCTGCTGTGATGT 540
Db 481 AGTCTAAATGGCTTAAATGGGAAACTGTTACCTGCTGTGATGT 540

QY 541 GCTTAAATGGGAAACTGTTACCTGCTGTGATGT 600
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QY 601 TTACAGAAATTGACATTAAATGGGATACTGTTAAATGGGATACTTAAAGG 660
Db 601 TTACAGAAATTGACATTAAATGGGATACTGTTAAATGGGATACTTAAAGG 660

QY 661 AAGATGACAGGGAAAGGAAGGAAAGTGTGCCAAGAAAAAAA 713
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RESULT 509
US-10-147-516-473

Sequence 473, Application US/10147536
Publication No. US20040077064A1

GENERAL INFORMATION:

- APPLICANT: Baker, Kevin P.
- APPLICANT: Beresini, Maureen
- APPLICANT: DeForge, Laura
- APPLICANT: Desnoyers, Luc
- APPLICANT: Filivroff, Ellen
- APPLICANT: Gao, Wei-Qiang
- APPLICANT: Gerritsen, Mary E.
- APPLICANT: Goddard, Audrey
- APPLICANT: Godowski, Paul J.
- APPLICANT: Gurney, Austin L.
- APPLICANT: Sherwood, Steven

RESULT 510

US-10-270-470-5
; Sequence 5, Application US/10270470
; Publication No. US20030162955A1
GENERAL INFORMATION:
; APPLICANT: Chalus, Lionel
; APPLICANT: Quan, Ann B.
; APPLICANT: Bates, Elizabeth Ester Mary
; APPLICANT: Goran, Daniel M.
; APPLICANT: Saeland, Sem
; Lebecque, Serge J.E.
; APPLICANT: Phillips, Joseph H.
TITLE OF INVENTION: ISOLATED MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
FILE REFERENCE: DX0802QK
CURRENT APPLICATION NUMBER: US/10/270,470
CURRENT FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: US 09/270,368
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: US 60/078,334
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 1018
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
; NAME/KEY: CDS
; LOCATION: (160)..(900)
; OTHER INFORMATION:
US-10-270-470-5

Query Match Score 140; DB 1; Length 1018;
Best Local Similarity 100.0%; Pred. No. 3 5e+02;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 361 GCTATTGGAGATCCAAATTGAGGAAACACATTGGAGATGGTACTTTCTATCAAGA 420
Qy 194 AATAAGAGAACACAGTCACACCCACACATCATCTTAGAACAGACTGTGACTCCTAAC 253
Db 421 AATAAGAGAACACAGTCACACCCACACATCATCTTAGAACAGACTGTGACTCCTAAC 480
Qy 254 AAAGCTGTCAAACCAACAGG 273
Db 481 AAAGCTGTCAAACCAACAGG 500

Search completed: June 2, 2004, 16:49:49
Job time : 184 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 2, 2004, 16:18:53 ; Search time 227 Seconds

3.966 Million cell updates/sec

Title: US-09-989-293A-376

Perfect score: 713
Sequence: 1 aatatacatctattatca.....tgtgccaaggaaaaaaa 713

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 8 seqs, 631314 residues

Total number of hits satisfying chosen parameters: 16

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 8 summaries

Database : rge376.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	713	100.0	713	1	AR252626		ACCESSION: AR252626
2	713	100.0	713	1	AX055452		ACCESSION: AX055452
3	713	100.0	713	1	AX03489		ACCESSION: AX03489
4	713	100.0	713	1	AX64340		ACCESSION: AX64340
5	713	100.0	713	1	AY58685		ACCESSION: AY58685
C	6	705.6	99.0	1	AC024224		ACCESSION: AC024224
C	7	594.7	83.4	240864	AC006510		ACCESSION: AC006510
C	8	211.499	29.7	221471	AC138620		ACCESSION: AC138620

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
AR252626	AR252626	Sequence 376 from patent US 6,788,25.	713 bp	DNA		AX055452			PAT 20-DEC-2002	
						Sequence 82 from Patent WO073452.				
						ACCESSION AX055452				
						VERSION GI:12228719				
						KEYWORDS				
						SOURCE Homo sapiens (human)				
						ORGANISM Homo sapiens				
						Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
						REFERENCE 1				
						AUTHORS Ashkenazi, A.J., Baker, K.P., Chan, B., Goddard, A., Gurney, A.L., Hebert, C., Henzel, W., Kabakoff, R.C., Shelton, D.L., Tumas, D., Watanabe, C.K. and Wood, W.I.				
						TITLE Compositions and methods for the treatment of immune related diseases				
						PATENT WO 0073452-A 82 07-DEC-2000;				
						Genentech, Inc (US)				
						LOCATION/QUALIFIERS Location/Qualifiers				
						FEATURES mol_type="genomic DNA"				

source	1. .713 /mol type="Homo sapiens" /db_xref="taxon:3606"	TITLE Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K., Williams,P., Wood,W.J. and Zhang,Y. Secreted and transmembrane polypeptides and nucleic acids encoding the same
Query Match	100.0% Score 713; DB 1; Length 713; Best Local Similarity 100.0%; Pred. No. 4.7; Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	JOURNAL Patent: WO 0073454-A 376 07-DEC-2000; Genentech Inc. (US) Location/Qualifiers
FEATURES	source	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
Qy	1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60	Query Match 100.0% Score 713; DB 1; Length 713; Best Local Similarity 100.0%; Pred. No. 4.7; Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60	JOURNAL 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60
Qy	61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120	FEATURES 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60
Db	61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120	source 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
Qy	121 GTGGTATGGAGCTATTGGAGTCATTCAAGGAACATGGAGAAGTGGCA 180	Query Match 100.0% Score 713; DB 1; Length 713; Best Local Similarity 100.0%; Pred. No. 4.7; Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	121 GTGGTATGGAGCTATTGGAGTCATTCAAGGAACATGGAGAAGTGGCA 180	JOURNAL 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60
Qy	181 CTTCTPATCAGAAATAAGAGAACCAACCACAGCAACAGCAACAGTC 240	FEATURES 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
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Qy	241 TGTGACTCTPACCAAAAGCTCTCAAACACACAGCAAGGGCAATGAACT 300	Query Match 100.0% Score 713; DB 1; Length 713; Best Local Similarity 100.0%; Pred. No. 4.7; Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	241 TGTGACTCTPACCAAAAGCTCTCAAACACACAGCAACAGGC 240	JOURNAL 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60
Qy	301 TGACTCAAGGGTTAATTCTGGCTGCTGAGCCTGGCAGGGCTGTAAAGAAC 360	FEATURES 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
Db	301 TGACTCAAGGGTTAATTCTGGCTGCTGAGCCTGGCAGGGCTGTAAAGAAC 360	source 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
Qy	361 TTAGATTCAATGATGTAATTAGCAATACTATTAGTAACTCTTAGTAACT 420	Query Match 100.0% Score 713; DB 1; Length 713; Best Local Similarity 100.0%; Pred. No. 4.7; Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	361 TTAGATTCAATGATGTAATTAGCAATACTATTAGTAACTCTTAGTAACT 420	JOURNAL 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60
Qy	421 GTATCCCTGTCTATATACATAATAGCTGAAATTATACTGCTGAC 480	FEATURES 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
Db	421 GTATCCCTGTCTATATACATAATAGCTGAAATTATACTGCTGAC 480	source 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
Qy	481 AGTTCTAAATGGACTTTAAATCTGTAATCTGGCTATGT 540	Query Match 100.0% Score 713; DB 1; Length 713; Best Local Similarity 100.0%; Pred. No. 4.7; Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	481 AGTTCTAAATGGACTTTAAATCTGTAATCTGGCTATGT 540	JOURNAL 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 60
Qy	541 GCTTAGATCAAGGAGTCAATATATTGATACAATGTTAATGATGAAAG 600	FEATURES 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
Db	541 GCTTAGATCAAGGAGTCAATATATTGATACAATGTTAATGATGAAAG 600	source 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
Qy	601 TTACGAAATTGACATTAAATGGATACATGTTAATGATGAAATGATGAAAG 660	Query Match 100.0% Score 713; DB 1; Length 713; Best Local Similarity 100.0%; Pred. No. 4.7; Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	601 TTACGAAATTGACATTAAATGGATACATGTTAATGATGAAATGATGAAAG 660	JOURNAL 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 600 1 AATATATCATCTATTATTAATGATTCAATTAACATTTTATCCATAAACATTGGG 600
Qy	661 AAGATGACAGGGAGAAGGGAAAGGAAAGGGAAAATGTGCCAAGGAAAAAAA 713	FEATURES 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
Db	661 AAGATGACAGGGAGAAGGGAAAGGAAAGGGAAAATGTGCCAAGGAAAAAAA 713	source 61 TTTCGGATTAAATTCAAACAGCAATGCAATTTCGTCATTATTATT 120
RESULT 3	AX403489	RESULT 4
LOCUS	AX403489	AX464340
DEFINITION	Sequence 376 from Patent WO0073454.	LOCUS AX464340
ACCESSION	AX403489	DEFINITION Sequence 473 from Patent WO0140466.
VERSION	AX403489.1	VERSION AX464340
KEYWORDS	GI:21436980	KEYWORDS
SOURCE	Homo sapiens (human)	SOURCE Homo sapiens
ORGANISM	Homo sapiens	ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D., Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P., Grimaldi,C.J., Gurney,A.L., Klijaviv,I., Napier,M.A., Pan,J.,	REFERENCE 1 GI:21899186

ORGANISM	Homo sapiens	LOCUS	AY358685	713 bp mRNA linear	PRI 03-OCT-2003
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens clone DNA60627 CLECSF12 (UNQ589) mRNA, complete cds.	DEFINITION	Homo sapiens		
REFERENCE	1	ACCESION	AY358685		
AUTHORS	Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Geritsen, M.E., Goddard, A., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.	VERSION	AY358685.1	GI:37182491	
FEATURES	source	KEYWORDS	FBI CDNA, Homo sapiens (human)		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding same	ORGANISM	Homo sapiens		
JOURNAL	Patent: WO 0140466-A 473 07-JUN-2001; Genentech Inc. (US)	REFERENCE 1	(bases 1 to 713)		
FEATURES	Location/Qualifiers	AUTHORS	Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Currey, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P.E., Heidens, S., Huang, A., Kim, H.S., Klomski, L., Lee, J., Lewis, J., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Zhang, Z., Xie, M.H., Yasura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, N.I. and Godowski, P.		
source	1..713 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	REFERENCE 2	(bases 1 to 713)		
Query Match Score 713; DB 1; Length 713;	TITLE	REFERENCE 3	(bases 1 to 713)		
Best Local Similarity 100.0%; Pred. No. 4.7;	JOURNAL	AUTOHRS	(bases 1 to 713)		
Matches 713; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	JOURNAL	Direct Submission			
Db	1 AAATATATCATCTATTATCAATAATCATTATTCTTATTCCAAATACATTGGG 60	JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		
Db	1 AAATATATCATCTATTATCAATAATCATTATTCTTATTCCAAATACATTGGG 60	FEATURES	Location/Qualifiers		
Qy	61 TTGGGATTTTAATTTCAAACAGCGGAATGACATTTCCTGTCACTATTATT 120	source	1..713		
Db	61 TTGGGATTTTAATTTCAAACAGGAATGACATTTCCTGTCACTATTATT 120	/organism="Homo sapiens"			
Qy	121 GTGGTATGTAAGGTCAATTGGATGCCAACATGGAGAACATGGGCTA 180	/mol type="mRNA"			
Db	121 GTGGTATGTAAGGTCAATTGGATGCCAACATGGAGAACATGGGCTA 180	/db_xref="mRNA:9606"			
Qy	181 CTTCCTATAGATAAGAACACAGTCACCCACATCATCTTGAGACAG 240	gene	1..713		
Db	181 CTTCCTATAGATAAGAACACAGTCACCCACATCATCTTGAGACAG 240	CDS	92..364		
Qy	241 TGACTCTTCAAAGCTGTCAAACCAAGGGCATAGTTAAAGGGGAATCT 300	/locus_tag="UNQ589"			
Db	241 TGACTCTTCAAAGCTGTCAAACCAAGGGCATAGTTAAAGGGGAATCT 300	/codon_start=1			
Qy	301 TGACTCAAGAGGGTTAAATTCTGGTGTGAAAGCCTGGGCAAGGGCATA 360	/product="CLECSF12"			
Db	301 TGACTCAAGAGGGTTAAATTCTGGTGTGAAAGCCTGGGCAAGGGCATA 360	/protein_id="AAQ89048.1"			
Qy	361 TTAGATTCATGATTGTAATTAAAGGAAATACACATCTTGTGAAAT 420	/db_xref="GI:37182492"			
Db	361 TTAGATTCATGATTGTAATTAAAGGAAATACACATCTTGTGAAAT 420	/translation="MFTEFLSLLLVCEATWRSNSGSNTDENGYELUSRNKENHSOPTQSSLEDSVTPTKAVKTGKGIVKGRNLDSRLILGAEAWGRGVKNT"			
Qy	481 AGTCTTAATTGGGACTTATTAAATCTGGTAAATGTTAATCTGGTGTGG 480	Query Match Score 713; DB 1; Length 713;			
Db	481 AGTCTTAATTGGGACTTATTAAATCTGGTAAATGTTAATCTGGTGTGG 480	Best Local Similarity 100.0%; Pred. No. 4.7;			
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Qy	301 TGACTCAAGGGTTAAATTCTGGTGTGAAAGCTGGCAAGGGTAAAGAACAC 360	Qy	181 CTTCTATCAAGAAATAGAGAACATGACATCTTGAAGACAG 240		
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Db	301	TGACTCAAAGGGTTAATTCTTGGTGTAAAGCTGGGAGGGTGAAGAAAAAC	360	Scherer,S., Scott,G., Shen,H., Shim,C., Shooshtari,N., Sissoon,I., Soderren,E., Sonaike,T., Sparks,A., Stanely H., Stone H., Sutton,A., Svatek,A., Taylor,P., Tamerisa A., Tang,H., Tansey,J., Taylor,C., Taylor,R., Telford,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villaon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wilecyk,R., Wooden,S., Worley,K., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R., Weinstock,G., and Gibbs,R.
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DEFINITION	Homo sapiens 12 BAC RP1-133L14 (Roswell Park Cancer Institute Human BAC Library)	complete sequence.		
ACCESSION	AC024224			
VERSION	AC024224.33	GI:21240476		
KEYWORDS	HTGC.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	1 (bases 1 to 165414)			
AUTHORS	Muzny D.M., Adams,S.L., Adio-Oduola,B., Ali-Osman,F.R., Allen,C., Alisbrooks,S.L., Amaraltinge,H.C., Are,J.R., Ayale,M., Banks,T., Barberia,J., Benton,J., Binage,K., Blonkenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieve,M., Brown,E., Brown,M., Bryant,N.P., Butay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,F., Carter,M., Cavazos,S.R., Chiu,D., Chowdhry,I., Christopoulou,C., Chen,G., Chen,R., Chen,Z., Chiu,D., Coyle,M.D., Dathorne,S.R., David,R., Cleveland,C.D., Cox,C., Davy-Carroll,L., Dederich,D.A., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Dunn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Escott,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Hart,M., Havlik,P., Hayes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,J., Hollins,B., Honsi,F., Howard,J., Huber,J., Hulyk,S., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovari,C., Kratovic,J., Kureishi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Lousegd,H., Lozado,R.J., Lu,X., Matondel,I., Martin,R., Marrindale,A., Martinez,E., Massey,E., Mashiney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S., Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Neal,D., Nelson,D., Newton,J., Nguyen,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokonko,S., Ogur,M., Okwundu,G., Oraclune,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,			
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DEFINITION	Homo sapiens clone RP11-13C13, RP11
PROGRESS ***	, 16 unordered pieces.
ACCESSION	AC006510 AC00510
VERSION	AC006510..8 GI:10122018
KEYWORDS	HTG; HTGS; PHASEII; Homo sapiens (human)

ORGANISM	Homo sapiens
MATERIAL	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 240864)
AUTHORS	Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaralatunge, H.C., Are, J.R., Banks, T., Barbour, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Bryant, N.P., Buhay, J., Burkhart, C., Burkett, C., Burriel, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J.J., Chavez, D.J., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleve, Land, C.D., Cox, C., Coyle, M.D., Datphorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earhart, C., Edgar, D., Edwards, C.C., Elnahaj, C., Escoto, M.M., Flores, T., Ferraguto, D., Flagg, N., Ford, J.U., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrelle, J.H., Guavara, A., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, R., Hodson, A., Hoques, M., Holloway, C., Hollands, B., Homsi, F., Howard, S., Huber, J., Huynh, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jouhar, S., Karsson, E., Kelly, S., Khan, U., King, L., Koray, J., Kovari, C., Kratovic, J., Kuroishi, A., Landry, N., Leal, B., Lewis, J., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H., Lorado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mayhiney, E., McLeod, M.P., Meadow, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Moabat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtonson, J., Newstrom, N., Nguyen, A., Nguyen, N.N., Nguyen, N., Nickerson, E., Nwokenwo, S., Ogwu, M., Okuongwa, G., Oragnye, N., Oviledo, R., Pace, A., Peery, J., Perez-L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojibutan, I., Rose, M., Ruisz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoothartari, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerrisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Tellier, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wieczyk, R., Woeden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., and Gibbs, R.
TITLE	Unpublished
JOURNAL	2 (bases 1 to 240864)
REFERENCE	Worley, K.C.
AUTHORS	Worley, K.C.
JOURNAL	Direct Submission
COMMENT	Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 14, 2000 this sequence version replaced q1:10086352. ----- Genome Center Center: Baylor College of Medicine Center code: BCM Web site: http://www.lgscc.bcm.tmc.edu/ Contact: hgsch-help@bcm.tmc.edu ----- Project Information Center project name: U-33 Center clone name: RP11-13C3, RP11-656E20 ----- Summary Statistics Sequencing vector: Plasmid: M77789 Sequencing vector: M13; L08821 Chemistry: Dye-primer Bodipy: 77% of reads Chemistry: Dye-terminator Big Dye: 23% of reads Assembly program: Phrap: version 0.990329 Consensus quality: 93±0.4 bases at least Q30 Consensus quality: 11±0.7 bases at least Q20 Estimated insert size: 229±0.1; sum-of-contigs estimation Estimated insert size: 331±0.00; agarose-fp estimation Consensus quality: 71±0.9 bases at least Q40 Quality coverage: 0.6x in Q20 bases; agarose-fp estimation Quality coverage: 0.9x in Q20 bases; sum-of-contigs estimation

REFERENCE
 AUTHORS McPherson, J.D. and Waterston, R.H.
 TITLE The sequence of *Mus musculus* clone
 JOURNAL Unpublished
 REFERENCE
 AUTHORS McPherson, J.D. and Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (12-JAN-2003) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 REFERENCE
 AUTHORS McPherson, J.D. and Waterston, R.H.
 TITLE Direct Submission
 JOURNAL Submitted (25-FEB-2003) Genome Sequencing Center, 4444 Forest Park
 Parkway, St. Louis, MO 63108, USA
 COMMENT On Feb 25, 2003 this sequence version replaced gi:27657609.

----- Genome Center -----
 Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site:<http://genome.wustl.edu/gsc/index.shtml>
 Contact: submissions@wustl.edu

----- Project Information -----
 Center project name: M_BA250E01

----- Summary Statistics -----
 Sequencing vector: M13; 0%
 Sequencing vector: Plasmid; 100%
 Chemistry: Dye-primer ET; 0% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 217739 bases at least Q40
 Consensus quality: 218068 bases at least Q30
 Consensus quality: 218373 bases at least Q20

Insert size: 193000; agarose-fp
 Insert size: 227102; sum-of-contigs
 Quality coverage: 14.88 in 020 bases; agarose-fp
 Quality coverage: 12.33 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 13 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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 * 3423: contig of 1814 bp in length
 * 3424 3523: gap of unknown length
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 * 8574 13990: contig of 5417 bp in length
 * 13991 14090: gap of unknown length
 * 14091 20220: contig of 6130 bp in length
 * 20320 20221: gap of unknown length
 * 33395: contig of 13075 bp in length
 * 33396: gap of unknown length
 * 33496 46731: contig of 13436 bp in length
 * 46732 46831: gap of unknown length
 * 46832 62518: contig of 15687 bp in length
 * 62618 62619: gap of unknown length
 * 62619 80892: contig of 18274 bp in length
 * 80893 80992: gap of unknown length
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Search completed: June 2, 2004, 16:22:42
Job time : 229 secs

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OM nucleic - nucleic search, using SW mode.

Run on: June 2, 2004, 16:29:06 ; Search time 54 Seconds

Perfect score: 713 (without alignments)

Sequence: 1 aatatatcatctattatac.....tgtggccaaagaaaaaaa 713

Title: US-09-989-293A-376
Scoring table: IDENTITY_NUC Gapext 0.5

Searched: 207 seqs, 152209 residues

Total number of hits satisfying chosen parameters: 414

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 207 summaries

Database : rng376.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	713	100.0	713	1	AAC58674		Human cDNA encoding membrane-bound protein PRO1159. Prot sequence.
3	713	100.0	713	1	AAS21480		Human PRO1159 (UNQ Human PRO Polynuc)
4	713	100.0	713	1	AAFA24240		Human PRO Polynuc
5	713	100.0	713	1	ABX71952		Novel human secreted membrane-bound protein ABX71952.
6	713	100.0	713	1	ABXB0364		Human cDNA encoding membrane-bound protein ABX71952.
7	713	100.0	713	1	ACA69270		Novel human secreted membrane-bound protein ABX71952.
8	713	100.0	713	1	ACD24089		Human secreted membrane-bound protein ABX71952.
9	713	100.0	713	1	ABX90141		Human secreted membrane-bound protein ABX71952.
10	713	100.0	713	1	ABX64187		Human secreted membrane-bound protein ABX71952.
11	713	100.0	713	1	ACDA67230		Novel human secreted membrane-bound protein ABX71952.
12	713	100.0	713	1	ACA64439		Novel human secreted membrane-bound protein ABX71952.
13	713	100.0	713	1	ACA03839		Novel human secreted membrane-bound protein ABX71952.
14	713	100.0	713	1	ABX9377		Novel human secreted membrane-bound protein ABX71952.
15	713	100.0	713	1	ABX80888		Novel human secreted membrane-bound protein ABX71952.
16	713	100.0	713	1	ACD42317		Novel human secreted membrane-bound protein ABX71952.
17	713	100.0	713	1	ACD4231		Novel human secreted membrane-bound protein ABX71952.
18	713	100.0	713	1	ABX79548		Novel human secreted membrane-bound protein ABX71952.
19	713	100.0	713	1	ACA93569		Novel human secreted membrane-bound protein ABX71952.
20	713	100.0	713	1	ABX81251		Novel human secreted membrane-bound protein ABX71952.
21	713	100.0	713	1	ACD814260		Novel human secreted membrane-bound protein ABX71952.
22	713	100.0	713	1	ACA93067		Novel human secreted membrane-bound protein ABX71952.
23	713	100.0	713	1	ABX17151		Novel human secreted membrane-bound protein ABX71952.
24	713	100.0	713	1	ACA68005		Novel human secreted membrane-bound protein ABX71952.
25	713	100.0	713	1	ACA88455		Novel human secreted membrane-bound protein ABX71952.
26	713	100.0	713	1	ACD81962		Novel human secreted membrane-bound protein ABX71952.
27	713	100.0	713	1	ADA45992		Novel human secreted membrane-bound protein ABX71952.
28	713	100.0	713	1	ADA76423		Novel human secreted membrane-bound protein ABX71952.
29	713	100.0	713	1	ADA19073		Novel human secreted membrane-bound protein ABX71952.
30	713	100.0	713	1	ADA61696		Novel human secreted membrane-bound protein ABX71952.
31	713	100.0	713	1	ADB19481		Novel human secreted membrane-bound protein ABX71952.
32	713	100.0	713	1	ADB28022		Novel human secreted membrane-bound protein ABX71952.
33	713	100.0	713	1	ADA86501		Novel human secreted membrane-bound protein ABX71952.

34	713	100.0	713	1	ADB16055	Human PRO polymuc
35	713	100.0	713	1	ADA37887	Human cDNA encodin
36	713	100.0	713	1	ADA47851	Human cDNA encodin
37	713	100.0	713	1	ADB21573	Human cDNA encodin
38	713	100.0	713	1	ADA10360	Human PRO polymuc
39	713	100.0	713	1	ADA67646	Human PRO polymuc
40	713	100.0	713	1	ADB30653	cDNA encoding huma
41	713	100.0	713	1	ADA85494	Novel human secret
42	713	100.0	713	1	ADA17904	cDNA encoding huma
43	713	100.0	713	1	ADA97161	Human PRO polymuc
44	713	100.0	713	1	ADA79465	Novel human secret
45	713	100.0	713	1	ADA87604	Human PRO polymuc
46	713	100.0	713	1	ADB16806	Human PRO polymuc
47	713	100.0	713	1	ADA28112	Novel human secret
48	713	100.0	713	1	ADA31898	Human cDNA encodin
49	713	100.0	713	1	ADA45992	Novel human secret
50	713	100.0	713	1	ADB18922	Human PRO polymuc
51	713	100.0	713	1	ADA54137	Novel human secret
52	713	100.0	713	1	ADB20033	Human PRO polymuc
53	713	100.0	713	1	ADA132356	Novel human secret
54	713	100.0	713	1	ACD38660	Novel human secret
55	713	100.0	713	1	ADA54592	Human PRO polymuc
56	713	100.0	713	1	ADA74599	Human PRO polymuc
57	713	100.0	713	1	ADA48332	Human PRO polymuc
58	713	100.0	713	1	ADA2356	Human PRO polymuc
59	713	100.0	713	1	ADA75319	Novel human secret
60	713	100.0	713	1	ADA5397	Novel human secret
61	713	100.0	713	1	ADA48450	Human cDNA encoding huma
62	713	100.0	713	1	ADA80101	Human PRO polymuc
63	713	100.0	713	1	ADA80629	Human PRO polymuc
64	713	100.0	713	1	ADA5871	Human cDNA encoding huma
65	713	100.0	713	1	ADA38817	Human PRO polymuc
66	713	100.0	713	1	ADA7096	Human PRO polymuc
67	713	100.0	713	1	ADB25392	Human cDNA encoding huma
68	713	100.0	713	1	ADA3568	Human PRO polymuc
69	713	100.0	713	1	ADB26918	Human cDNA encoding huma
70	713	100.0	713	1	ADB31205	Human cDNA encoding huma
71	713	100.0	713	1	ADA52938	Human cDNA encoding huma
72	713	100.0	713	1	ADA61133	Human cDNA encoding huma
73	713	100.0	713	1	ADA56609	Human PRO polymuc
74	713	100.0	713	1	ADA81181	Human PRO Polymuc
75	713	100.0	713	1	ADA96057	Human PRO Polymuc
76	713	100.0	713	1	ADB26366	Human PRO Polymuc
77	713	100.0	713	1	ADB21851	Human PRO Polymuc
78	713	100.0	713	1	ADA77630	Human cDNA encoding huma
79	713	100.0	713	1	ADB18370	Human cDNA encoding huma
80	713	100.0	713	1	ADA87053	Novel human secret
81	713	100.0	713	1	ADA88156	Novel human secret
82	713	100.0	713	1	ADA88108	Novel human secret
83	713	100.0	713	1	ADA45544	Human PRO Polymuc
84	713	100.0	713	1	ADB28574	Human cDNA encoding huma
85	713	100.0	713	1	ADA23126	Human cDNA encoding huma
86	713	100.0	713	1	ACH6523	Human PRO Polymuc
87	713	100.0	713	1	ADA77078	Human cDNA encoding huma
88	713	100.0	713	1	ADA22499	Human cDNA encoding huma
89	713	100.0	713	1	ADA88108	Novel human secret
90	713	100.0	713	1	ADA97113	Human PRO Polymuc
91	713	100.0	713	1	ADB22740	Novel human secret
92	713	100.0	713	1	ADB22403	Human PRO Polymuc
93	713	100.0	713	1	ACD39513	Novel human secret
94	713	100.0	713	1	ADA66655	Human PRO Polymuc
95	713	100.0	713	1	ADA39558	Novel human secret
96	713	100.0	713	1	ADA67094	Human PRO Polymuc
97	713	100.0	713	1	ADB2255	Novel human secret
98	713	100.0	713	1	ADB23128	Human PRO Polymuc
99	713	100.0	713	1	ADA97450	Novel human secret
100	713	100.0	713	1	ADB1513	Human PRO Polymuc
101	713	100.0	713	1	ADA88165	Novel human secret
102	713	100.0	713	1	ADB96384	Human PRO Polymuc
103	713	100.0	713	1	ADB38613	Novel human secret
104	713	100.0	713	1	ADB6685	Novel human secret
105	713	100.0	713	1	ADB89765	Human PRO Polymuc
106	713	100.0	713	1	ADB90497	Human PRO Polymuc

107	713	100.0	ADB39598	Novel human secret	Human PRO Polynuc1	180	713	100.0	713	1	ADE19579
108	713	100.0	ADB47221	Novel human secret	Human PRO Polynuc1	181	713	100.0	713	1	ADE19127
109	713	100.0	ADB86821	Human PRO Polynuc1	182	713	100.0	713	1	ADE41223	
110	713	100.0	ADB77433	Novel human secret	Human PRO Polynuc1	183	713	100.0	713	1	ADE98112
111	713	100.0	ADB34580	Human PRO Polynuc1	184	713	100.0	713	1	ADE22598	
112	713	100.0	ADB35694	Human PRO Polynuc1	185	713	100.0	713	1	ADE79116	
113	713	100.0	ADB4038	Human PRO Polynuc1	186	713	100.0	713	1	ADE26166	
114	713	100.0	ADB35142	Novel human secret	Novel human secret	187	713	100.0	713	1	ADE32466
115	713	100.0	ADB36245	Human PRO Polynuc1	188	713	100.0	713	1	ADE42558	
116	713	100.0	ADB46641	Novel human secret	CDNA encoding huma	189	713	100.0	713	1	ADD8074
117	713	100.0	ADC77856	Human PRO Polynuc1	190	713	100.0	713	1	ADD89102	
118	713	100.0	ADC55220	Human PRO Polynuc1	191	713	100.0	713	1	ADE40886	
119	713	100.0	ADC12087	Human cDNA encoding huma	192	713	100.0	713	1	ADE04185	
120	713	100.0	ADC65059	Human PRO Polynuc1	193	713	100.0	713	1	ADC81110	
121	713	100.0	ADC07569	Human cDNA encoding huma	194	713	100.0	713	1	ADD76558	
122	713	100.0	ADC11554	Human cDNA encoding huma	195	713	100.0	713	1	ADD88122	
123	713	100.0	ADC50514	Novel human secret	Human PRO Polynuc1	196	713	100.0	713	1	ADD86126
124	713	100.0	ADC72061	Novel human secret	Novel human secret	197	713	100.0	713	1	ADE7574
125	713	100.0	ADC60040	Novel human secret	Novel human secret	198	713	100.0	713	1	ADE23450
126	713	100.0	ADC53047	Novel human secret	Novel human secret	199	713	100.0	713	1	ADE24102
127	713	100.0	ADC57401	Novel human secret	Novel human secret	200	713	100.0	713	1	ADE2445
128	713	100.0	ADC60592	Novel human secret	Novel human secret	201	713	100.0	713	1	ADD87470
129	713	100.0	ADC51067	Novel human secret	Novel human secret	202	713	100.0	713	1	ADD89336
130	713	100.0	ADC65594	Human PRO Polynuc1	203	713	100.0	713	1	ADE1B75	
131	713	100.0	ADC54692	Novel human secret	Novel human secret	204	713	100.0	713	1	ADD88784
132	713	100.0	ADC5653	Novel human secret	Novel human secret	C 205	705.6	99.0	5709	1	AAK81882
133	713	100.0	ADC565176	Novel human secret	Novel human secret	C 206	701.5	98.4	712	1	AAK91811
134	713	100.0	ADC56054	Novel human secret	Novel human secret	C 207	332.8	46.7	336	1	AAK81884
135	713	100.0	ADC58624	Novel human secret	Novel human secret						
136	713	100.0	ADC14676	Novel human secret	Novel human secret						
137	713	100.0	ADD08208	Novel human secret	Novel human secret						
138	713	100.0	ADD03298	Novel human secret	Novel human secret						
139	713	100.0	ADC90290	Novel human secret	Novel human secret						
140	713	100.0	ADC82033	Human PRO Polynuc1	RESULT 1						
141	713	100.0	ADC69709	cDNA encoding huma	AAZ65594						
142	713	100.0	ADC48598	Human PRO Polynuc1	ID AAZ65094 standard; CDNA; 713 BP.						
143	713	100.0	ADD10127	Human PRO Polynuc1	XX						
144	713	100.0	ADD07675	Novel human secret	AAZ65094;						
145	713	100.0	ADD04705	Novel human secret	XX						
146	713	100.0	ADC82566	Novel human secret	DT 05-APR-2000 (first entry)						
147	713	100.0	ADC8033	Human PRO Polynuc1	XX						
148	713	100.0	ADC61165	cDNA encoding huma	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; gene mapping; 55.						
149	713	100.0	ADC48046	Human PRO Polynuc1	KW pharmaceutical; receptor immunoabsin; gene mapping; 55.						
150	713	100.0	ADD08746	Novel human secret	KW pharmaceutical; receptor immunoabsin; gene mapping; 55.						
151	713	100.0	ADC80106	Novel human secret	KW pharmaceutical; receptor immunoabsin; gene mapping; 55.						
152	713	100.0	ADD06995	Novel human secret	KW pharmaceutical; receptor immunoabsin; gene mapping; 55.						
153	713	100.0	ADD09575	Human PRO Polynuc1	XX						
154	713	100.0	ADC83242	Human PRO Polynuc1	PR 02-JUN-1998;						
155	713	100.0	ADD41288	Human PRO Polynuc1	PR 02-JUN-1998;						
156	713	100.0	ADD02427	Human PRO Polynuc1	PR 02-JUN-1998;						
157	713	100.0	ADD53167	CDNA encoding huma	PR 09-DEC-1999.						
158	713	100.0	ADD53719	Novel human secret	XX						
159	713	100.0	ADD55349	Human PRO Polynuc1	PR 02-JUN-1999;						
160	713	100.0	ADD56307	cDNA encoding huma	99WO-US012252.						
161	713	100.0	ADD51875	Human PRO Polynuc1	PR 02-JUN-1998;						
162	713	100.0	ADD02674	Human PRO Polynuc1	PR 02-JUN-1998;						
163	713	100.0	ADD02108	Human PRO Polynuc1	PR 02-JUN-1998;						
164	713	100.0	ADD54290	Novel human secret	PR 03-JUN-1998;						
165	713	100.0	ADD54745	Human PRO Polynuc1	PR 04-JUN-1998;						
166	713	100.0	ADD92607	Human PRO Polynuc1	PR 04-JUN-1998;						
167	713	100.0	ADD91503	Human PRO Polynuc1	PR 04-JUN-1998;						
168	713	100.0	ADE04117	Human PRO Polynuc1	PR 04-JUN-1998;						
169	713	100.0	ADE26899	Novel human secret	PR 04-JUN-1998;						
170	713	100.0	ADE37414	cDNA encoding huma	98US-008833P.						
171	713	100.0	ADE22346	cDNA encoding huma	98US-008833P.						
172	713	100.0	ADD9570	Human PRO Polynuc1	98US-008760P.						
173	713	100.0	ADD42106	Human PRO Polynuc1	98US-008760P.						
174	713	100.0	ADE17923	Human PRO Polynuc1	98US-008808P.						
175	713	100.0	ADD92055	Novel human secret	98US-008809P.						
176	713	100.0	ADE34518	cDNA encoding huma	98US-008655P.						
177	713	100.0	ADE34070	Novel human secret	98US-008872P.						
178	713	100.0	ADD80122	cDNA encoding huma	98US-008870P.						
179	713	100.0	ADD93159	Human PRO Polynuc1	98US-008873P.						

		17-APR-2002 ; 2002US-00124823.
QY	61	TTTGGGATTAACTTCAACAGGAATGACATTTCCTGCACTTATTATT 120
Db	61	TTTGGGATTAACTTCAACAGGAATGACATTTCCTGCACTTATTATT 120
QY	121	GTTGTATGTAAGCTATTGGAGATCCAAATTCCAGGACAACACATTGGAGATGGCTA 180
Db	121	GTTGTATGTAAGCTATTGGAGATCCAAATTCCAGGACAACACATTGGAGATGGCTA 180
QY	181	CTTCTATCAAGAAATAAGAACACAGTCACCCACATCATCTTGTAGACAG 240
Db	181	CTTCTATCAAGAAATAAGAACACAGTCACCCACATCATCTTGTAGACAG 240
QY	241	TGTGACTCCTACCAAGCTGTCAAACACAGGCAAGGCATAGTAAAGGACGAACT 300
Db	241	TGTGACTCCTACCAAGCTGTCAAACACAGGCAAGGCATAGTAAAGGACGAACT 300
QY	301	TGACTCAAGAGGGTAATTCTCGTGTGAAGCTGGCGAGGGTAAAGAAAACAC 360
Db	301	TGACTCAAGAGGGTAATTCTCGTGTGAAGCTGGCGAGGGTAAAGAAAACAC 360
QY	361	TTAGATICAATGATGCTAAATTAGCTAAATACACATATTAGTAACTGTAAAT 420
Db	361	TTAGATICAATGATGCTAAATTAGCTAAATACACATATTAGTAACTGTAAAT 420
QY	421	GTCATCCGTCTATATACTAACTAGCTGAAATTATACTGGCTGGAC 480
Db	421	GTCATCCGTCTATATACTAACTAGCTGAAATTATACTGGCTGGAC 480
QY	481	AGTCCTAAATGGACTTTAAATTAAATCAGTAACTGGCTATGTTACCTGTATGT 540
Db	481	AGTCCTAAATGGACTTTAAATTAAATCAGTAACTGGCTATGTTACCTGTATGT 540
QY	541	GCTTAGATCTACAGGAGTCATAATAATTGTATAAACTGGTACTGATTATCACTGGCTATGT 600
Db	541	GCTTAGATCTACAGGAGTCATAATAATTGTATAAACTGGTACTGATTATCACTGGCTATGT 600
QY	601	TTACAGAATTGACATTAAATCGATAACAGTTAGAAATATGACATTAGAAAGG 660
Db	601	TTACAGAATTGACATTAAATCGATAACAGTTAGAAATATGACATTAGAAAGG 660
QY	661	AAGATGACAGGGAGAAGGAGAAGGAAATTTGCCAAGAAAAAAA 713
Db	661	AAGATGACAGGGAGAAGGAGAAGGAAATTTGCCAAGAAAAAAA 713
	RESULT 202	
ID	ADE89336	Human gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.
XX	ADENINE	Homo sapiens.
XX	ADE89336 standard;	cDNA: 713 BP.
AC	ADE89336;	
XX	DT	29-JAN-2004 (first entry)
XX	DE	Human PRO polynucleotide #237.
XX	ID	ADE89336
XX	OS	
XX	PN	US2003199062-A1.
XX	VV	23-OCT-2003.

KW	liver; microvascular endothelial cell; glucose; FFA;
KW	skeletal muscle cell; adipocyte cell; pericyte cell;
KW	inner ear utricular supporting cell; T-lymphocyte cell;
KW	endothelial cell tube formation; bone disorder; cartilage disorder;
KW	sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW	rheumatoid arthritis; haemoglobin-associated disorder; thalassaemia;
KW	immune system cell infiltration.
XX	Home sapiens.
XX	US2003194794-A1.
EN	US2003194794-A1.
XX	16-OCT-2003 .
PD	PR 17-APR-2002; 2002US-00125805.
XX	PR 31-MAR-1997; 97WO-US005230.
PR	PR 12-JUN-1998; 98WO-US012456.
PR	PR 14-JUL-1998; 98WO-US014552.
PR	PR 18-AUG-1998; 98WO-US017888.
PR	PR 10-SEP-1998; 98WO-US016824.
PR	PR 14-SEP-1998; 98WO-US019093.
PR	PR 14-SEP-1998; 98WO-US019094.
PR	PR 14-SEP-1998; 98WO-US019177.
PR	PR 16-SEP-1998; 98WO-US019330.
PR	PR 17-SEP-1998; 98WO-US019437.
PR	PR 07-OCT-1998; 98WO-US021141.
PR	PR 29-OCT-1998; 98WO-US022291.
PR	PR 29-OCT-1998; 98WO-US022292.
PR	PR 20-NOV-1998; 98WO-US024495.
PR	PR 01-DEC-1998; 98WO-US025108.
PR	PR 05-JAN-1999; 99WO-US000106.
PR	PR 08-MAR-1999; 99WO-US005028.
PR	PR 10-MAR-1999; 99WO-US005190.
PR	PR 10-MAR-1999; 2000WO-US000319.
PR	PR 20-APR-1999; 99WO-US008615.
PR	PR 14-MAY-1999; 99WO-US010733.
PR	PR 02-JUN-1999; 99WO-US012252.
PR	PR 01-SEP-1999; 99WO-US020111.
PR	PR 08-SEP-1999; 99WO-US020534.
PR	PR 13-SEP-1999; 99WO-US020944.
PR	PR 15-SEP-1999; 99WO-US021190.
PR	PR 15-SEP-1999; 99WO-US021547.
PR	PR 05-OCT-1999; 99WO-US023089.
PR	PR 29-NOV-1999; 99WO-US028214.
PR	PR 30-NOV-1999; 99WO-US028313.
PR	PR 30-NOV-1999; 99WO-US028409.
PR	PR 01-DEC-1999; 99WO-US028501.
PR	PR 01-DEC-1999; 99WO-US028634.
PR	PR 02-DEC-1999; 99WO-US028551.
PR	PR 02-DEC-1999; 99WO-US028554.
PR	PR 02-DEC-1999; 99WO-US028565.
PR	PR 16-DEC-1999; 99WO-US030095.
PR	PR 20-DEC-1999; 99WO-US030911.
PR	PR 20-DEC-1999; 99WO-US030919.
PR	PR 22-DEC-1999; 99WO-US030920.
PR	PR 30-DEC-1999; 99WO-US031243.
PR	PR 30-DEC-1999; 99WO-US031244.
PR	PR 05-JAN-2000; 2000WO-US000219.
PR	PR 06-JAN-2000; 2000WO-US000277.
PR	PR 06-JAN-2000; 2000WO-US000376.
PR	PR 11-FEB-2000; 2000WO-US003565.
PR	PR 18-FEB-2000; 2000WO-US004341.
PR	PR 18-FEB-2000; 2000WO-US004342.
PR	PR 22-FEB-2000; 2000WO-US004414.
PR	PR 24-FEB-2000; 2000WO-US004914.
PR	PR 24-FEB-2000; 2000WO-US005004.
PR	PR 01-MAR-2000; 2000WO-US005601.
PR	PR 02-MAR-2000; 2000WO-US005746.
PR	PR 02-MAR-2000; 2000WO-US005841.
PR	PR 15-MAR-2000; 2000WO-US006884.
PR	PR 20-MAR-2000; 2000WO-US007337.
PR	PR 21-MAR-2000; 2000WO-US007532.

transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the Polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalasssemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdatab.uspto.gov/sequence.html.

XX

Sequence	713 BP; 262 A; 105 C; 134 G; 212 T; 0 U; 0 Other;	Score	713; DB 1; Length 713;
SQ		100.0%	
Query Match	100.0% ; Pred. No. 1.4;		
Best Local Similarity	100.0% ; Mismatches 0 ; Indels 0 ; Gaps 0 ;		
Matches	713 ; Conservative		
Qy	1 AATATACTCATTTATCATTAACTTAACTATGTTATTCCTTAATACATTGGGG	60	
Db	1 AAATATCACTTATCATTAACTTAACTATGTTATTCCTTAATACATTGGGG	60	
Qy	61 TTTCGGATTTTAATTCTAACACGCCAGATGACATTTTTCGTCACATTATTATT	120	
Db	61 TTTCGGATTTTAATTCTAACACGCCAGATGACATTTTTCGTCACATTATT	120	
Qy	121 GTGGTAGTGAACTATTGGAGATTCATTGGAACTTCAATTGGAAAGCACACATTGGCAATGGCTA	180	
Db	121 GTTGGTAGTGAACTATTGGAGATTCATTGGAACTTCAATTGGAAAGCACACATTGGCAATGGCTA	180	
Qy	181 CTTTCATTCAAGAAATAAGGAACCACGTAAACCACATCTTAAAGAACAG	240	
Db	181 CTTTCATTCAAGAAATAAGGAACCACGTAAACCACATCTTAAAGAACAG	240	
Qy	241 TGAGTCCATTCCAAGCTGCAAAACCAACAGGCCAAGGGCATAGTTAAAGGACGGAACT	300	
Db	241 TGAGTCCATTCCAAGCTGCAAAACCAACAGGCCAAGGGCATAGTTAAAGGACGGAACT	300	
Qy	301 TGACTCAAGGGTTATTCTGGCTGAAGCTGGGCAAGGGTTAAACAAACAC	360	
Db	301 TGACTCAAGGGTTATTCTGGCTGAAGCTGGGCAAGGGTTAAACAAACAC	360	
Qy	361 TTAGATTCATGTTGATTAATTAAGGCAAATACATATTAGTATTACTGTAAAT	420	
Db	361 TTAGATTCATGTTGATTAATTAAGGCAAATACATATTAGTATTACTGTAAAT	420	
Qy	421 AGTCATAATTGGACTTAAATTAAATCAGTAACCTATCATCTGCTATGT	540	
Db	421 GTATCCCTGTCATATACATATAAGGCGAAATTATAAGGCTCCTATGAGCTGGCAC	480	
PT	Novel secreted and transmembrane polypeptides, PRO useful for treating bone disorders, arthritis, heart attack, injuries, tumors, and stimulating release of TNF-alpha from human blood.		
PS	Claim 2; SEQ ID NO 473; 638pp; English.		

Db	481	AGTCTAAATTGGACTTTAATTAAATCGTAACCTGTTACTGGCTATGT	540	PR	01-SEP-2000;	20000US-0229343P.
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Db	541	GCTTAGATCTACAGGAGATCATATAATTGATACAAATAAAAGAAAAAGTCCTCC	600	PR	05-SEP-2000;	20000US-0229345P.
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QY	601	TTCAGAATTGCAATTTAATCGATACAGTTGAATGAAATTGACATTAGAAAGG	660	PR	06-SEP-2000;	20000US-0230437P.
Db	601	TTCAGAATTGCAATTTAATCGATACAGTTGAATGAAATTGACATTAGAAAGG	660	PR	08-SEP-2000;	20000US-0230438P.
QY	661	AAGATGACAGGGAAAGGAAATGTTGCCAGGAAAAAAA	713	PR	08-SEP-2000;	20000US-0231242P.
Db	661	AAGATGACAGGGAAAGGAAATGTTGCCAGGAAAAAAA	713	PR	08-SEP-2000;	20000US-0231243P.
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XX	PF 17-JAN-2001; 2001WO-US001354.			PR	14-SEP-2000;	20000US-0233066P.
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 PR 11-DEC-2000; 2000US-0254091P.
 PR 05-JAN-2001; 2000US-0259670P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

XX

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 36096; 3071pp + Sequence Listing; English.

AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAK64702 to AAK91921. (I) have cytosolic

activity, and can be used in gene therapy and vaccine production. (II)

proteins and polymuclootides may be used in the prevention, diagnosis and

treatment of diseases associated with inappropriate (I) expression. For

example, they may be used to treat disorders associated with decreased

expression, by rectifying mutations or deletions in a patient's genome

that affect the activity of (I) by expressing inactive proteins or to

CC supplement the patients own production of (I). Additionally, (I)
 CC polymyxoides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (II) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/haematopoietic-related diseases, especially
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/haematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.

XX Sequence 336 BP; 98 A; 66 C; 49 G; 123 T; 0 U; 0 Other;

SQ	46.7% ; Score 332.8 ; DB 1 ; Length 336;
Best Local Similarity 99.4% ; Pred. No. 98 ;	
Matches 334 ; Conservative 0 ; Mismatches 2 ; Indels 0 ; Gaps 0 ;	
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Db 276 GGTAATTCTGGTGGCTGAAGCCTGGGCAAGGGCTGAAAGAAAAACCTTAACTTCAATT 217	
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 Job time : 75 sec_B

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2004, 09:11:03 ; Search time 102 Seconds

(without alignments)
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Title: US-09-989-293A-376

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing First 65000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	75.2	10.5	528	3	US-08-772-440-7	Sequence 7, Appli
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c 4	45.2	6.3	832	4	US-09-792-2813	Sequence 2813, Ap
5	44	6.2	640681	4	US-09-790-988-1	Sequence 1, Appli
6	40.4	5.7	5847	4	US-09-920-672-10	Sequence 10, Appli
7	39.16	5.6	20674	4	US-09-641-638-651	Sequence 651, Appli
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9	39.2	5.5	8920	3	US-09-150-741-1	Sequence 2, Appli
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c 13	38.4	5.4	58407	4	US-08-916-421B-2	Sequence 2, Appli
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c 17	37.6	5.3	1335	4	US-09-743-661A-1450	Sequence 1450, Ap
c 18	37.4	5.2	275	4	US-08-885-593A-42	Sequence 42, Appli
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c 32	3.6	5.2	19124	2	US-08-487-826B-13	Sequence 13, Appli
c 33	3.6	5.1	10640	4	US-09-417-45D-5	Sequence 5, Appli
c 34	3.6	5.1	11131	3	US-10-204-708-27	Sequence 27, Appli
c 35	3.6	5.1	51952	3	US-08-947-823-1	Sequence 1, Appli
c 36	3.6	5.1	408	4	US-09-134-001C-1464	Sequence 1464, Ap
c 37	3.6	5.1	1946	4	US-09-886-319A-33	Sequence 83, Appli
c 38	3.6	5.1	3331	3	US-09-042-785A-1	Sequence 1, Appli
c 39	3.6	5.1	161652	4	US-09-497-855A-40	Sequence 40, Appli
c 40	3.6	5.1	6113	4	US-10-204-708-14	Sequence 14, Appli
c 41	3.6	5.0	6317	4	US-10-204-708-11	Sequence 11, Appli
c 42	3.6	5.0	11050	4	US-10-204-708-86	Sequence 86, Appli
c 43	3.6	5.0	50000	4	US-09-146-053-3	Sequence 3, Appli
c 44	35.8	5.0	1634	4	US-09-220-332-111	Sequence 111, Appli
c 45	35.8	5.0	2570	2	US-09-056-075-2	Sequence 2, Appli